Sequence Listing

- <110> Goddard, Audrey
 Godowski, Paul J.
 Gurney, Austin L.
 Watanabe, Colin K.
 Wood, William I.
- <120> NOVEL POLYPEPTIDES HAVING SEQUENCE SIMILARITY TO CYTOKINE RECEPTORS AND NUCLEIC ACIDS ENCODING THE SAME
- <130> P3121R1
- <140> US 09/964,994
- <141> 2001-09-26
- <150> PCT/US00/08439
- <151> 2000-03-30
- <150> PCT/US01/06520
- <151> 2001-02-28
- <150> US 60/191,015
- <151> 2000-03-21
- <150> US 09/941,992
- <151> 2001-08-28
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- ctcggctggg agctactcag aatggagcat gacgccgcgg ttcactccct 700





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Gln Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln
35 40 45

Trp Gln Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe
50 55 60

Val Gln Tyr Lys Ile Met Phe Ser Cys Ser Met Lys Ser Ser His
65 70 75

Gln Lys Pro Ser Gly Cys Trp Gln His Ile Ser Cys Asn Phe Pro 80 85 90

Gly Cys Arg Thr Leu Ala Lys Tyr Gly Gln Arg Gln Trp Lys Asn 95 100 105

Lys Glu Asp Cys Trp Gly Thr Gln Glu Leu Ser Cys Asp Leu Thr 110 115 120

Ser Glu Thr Ser Asp Ile Gln Glu Pro Tyr Tyr Gly Arg Val Arg 125 130 135

Ala Ala Ser Ala Gly Ser Tyr Ser Glu Trp Ser Met Thr Pro Arg

Phe Thr Pro Trp Trp Glu Thr Lys Ile Asp Pro Pro Val Met Asn 155 160 165 $\widehat{}$

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Ile Thr Gln Val Asn Gly Ser Leu Leu Val Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn Val Ser Ile Glu 190 Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile Asn Asn Ser 205 210 Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu 250 255 Glu Arg Cys Val Glu Ile Pro <210> 3 <211> 27 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400> 3 ctggcaacag cagtgtctat tttgtgc 27 <210> 4 <211> 21 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400> 4 taagtgccct cccaggctgc c 21 <210> 5 <211> 52 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe tcctccagtc atgaatataa cccaagtcaa tggctctttg ttggtaattc 50 tc 52 <210> 6 <211> 1705 <212> DNA <213> Homo Sapien <400> 6 tgaaatgact tccacggctg ggacgggaac cttccaccca cagctatgcc 50





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Val Val Leu Pro Cys Leu Gly Phe Thr Leu Leu Leu Trp Ser Gln
35 40 45

Val Ser Gly Ala Gln Gly Gln Glu Phe His Phe Gly Pro Cys Gln
50 55 60

Val Lys Gly Val Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala 65 70 75

Val Lys Asp Thr Met Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg 80 85 90

Leu Leu Gln Gln Glu Val Leu Gln Asn Val Ser Asp Ala Glu Ser 95 100 105

Cys Tyr Leu Val His Thr Leu Leu Glu Phe Tyr Leu Lys Thr Val 110 115 120

Phe Lys Asn His His Asn Arg Thr Val Glu Val Arg Thr Leu Lys
125 130 135

Ser Phe Ser Thr Leu Ala Asn Asn Phe Val Leu Ile Val Ser Gln
140 145 150

Leu Gln Pro Ser Gln Glu Asn Glu Met Phe Ser Ile Arg Asp Ser 155 160 165

Ala His Arg Arg Phe Leu Leu Phe Arg Arg Ala Phe Lys Gln Leu 170 175 180

Asp Val Glu Ala Ala Leu Thr Lys Ala Leu Gly Glu Val Asp Ile 185 190 190

Leu Leu Thr Trp Met Gln Lys Phe Tyr Lys Leu 200 205